36



## SEQUENCE LISTING

<110> Xia, Yu-Ping et al.

- <120> METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
- <130> REG 710b
- <140> 09/773,877
- <141> 2001-01-31
- <160> 27
- <170> PatentIn version 3.0
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						agc Ser										240
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_		_				ggc Gly			_	_						336
			_	_	_	gaa Glu		_								384
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			_			gga Gly										480
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_			_			cgc Arg				_	_	_		_	_	576
				_	_	tac Tyr		_					_			624
_		_				ttg Leu 215									cga Arg	<sub>.</sub> 672
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	_													ggc Gly 335	gag Glu	1008	
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cca	gcc	ccc	atc	gag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	CCC	cga	1392	

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Pro	Ala 450	Pro	Ile	Glu	Lys	Thr 455	Ile	Ser	Lys	Ala	Lys 460	Gly	Gln	Pro	Arg	
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	cag Gln															1488
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Glu Leu Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr 35 40 45

Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr Ala Gln Ala Asn His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val Pro Thr Ser Lys Lys Glu Thr Glu Ser Ala Ile Tyr Ile Phe Ile Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Lys Asn Lys Arg Ala Ser Val Arg Arg Ile Asp Gln Ser Asn Ser His

275 280 285

Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys Ser Val Asn Thr Ser Val His Ile Tyr Asp Lys Ala Gly Pro Gly Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys 

520 525 515 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser 540 535 530 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser 560 555 545 550 Leu Ser Leu Ser Pro Gly Lys 565 <210> 13 <211> 1674 <212> DNA <213> Artificial <220> <223> Mut 1 <220> <221> CDS <222> (1)..(1674) <400> 13 atg gtc agc tac tgg gac acc ggg gtc ctg ctg tgc gcg ctg ctc agc 48 Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser 15 10 1 tgt ctg ctt ctc aca gga tct agt tca ggt tca aaa tta aaa gat cct 96 Cys Leu Leu Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys Asp Pro 30 20 25 gaa ctg agt tta aaa ggc acc cag cac atc atg caa gca ggc cag aca 144 Glu Leu Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr 35 40 ctg cat ctc caa tgc agg ggg gaa gca gcc cat aaa tgg tct ttg cct 192 Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro 50 55 60 gaa atg gtg agt aag gaa agc gaa agg ctg agc ata act aaa tct gcc 240 Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala 70 75 80 65

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser

						caa Gln										288
						ggc Gly									gta Val	336
cct Pro	act Thr	tca Ser 115	aag Lys	aag Lys	aag Lys	gaa Glu	aca Thr 120	gaa Glu	tct Ser	gca Ala	atc Ile	tat Tyr 125	ata Ile	ttt Phe	att Ile	384
						ttc Phe 135										432
						gga Gly										480
_						gtt Val										528
_						cgc Arg								-	_	576
				_		tac Tyr		_								624
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						gat Asp										720
			_			act Thr		_								768
						caa Gln										816
_		_				gcc Ala									_	864
_		_	-			gac Asp 295										912
_						tct Ser	_									960

305					310					315					320	
											aaa Lys					1008
											ccg Pro					1056
ttc Phe	ccc Pro	cca Pro 355	aaa Lys	ccc Pro	aag Lys	gac Asp	acc Thr 360	ctc Leu	atg Met	atc Ile	tcc Ser	cgg Arg 365	acc Thr	cct Pro	gag Glu	1104
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											aaa Lys					1344
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	_		_		_		_	_	_	_	acc Thr			_		1440
				Ser	_	Ile	Ala	Val	Glu	Trp	gag Glu	Ser	Asn			1488
_					_						ctg Leu				_	1536
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_			_			_		-	_		gag Glu 540					1632

1674

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Glu Leu Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr 35 40 45

Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro 50 60

Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala
65 70 75 80

Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr 85 90 95

Ala Gln Ala Asn His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val 100 105 110

Pro Thr Ser Lys Lys Glu Thr Glu Ser Ala Ile Tyr Ile Phe Ile 115 120 125

Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu 130 135 140

Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val
145 150 155 160

Thr	Ser	Pro	Asn	Ile 165	Thr	Val	Thr	Leu	Lys 170	_	Phe	Pro	Leu	Asp 175	
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Ile	Ile	Ser 195		Ala	Thr	Tyr	Lys 200	Glu	Ile	Gly	Leu	Leu 205	Thr	Cys	Glu
Ala	Thr 210	Val	Asn	Gly	His	Leu 215	Tyr	Lys	Thr	Asn	Tyr 220	Leu	Thr	His	Arg
Gln 225	Thr	Asn	Thr	Ile	Ile 230	Asp	Val	Gln	Ile	Ser 235	Thr	Pro	Arg	Pro	Val 240
Lys	Leu	Leu	Arg	Gly 245	His	Thr	Leu	Val	Leu 250	Asn	Cys	Thr	Ala	Thr 255	Thr
Pro	Leu	Asn	Thr 260	Arg	Val	Gln	Met	Thr 265	Trp	Ser	Tyr	Pro	Asp 270	Glu	Ile
Asp	Gln	Ser 275	Asn	Ser	His	Ala	Asn 280	Ile	Phe	Tyr	Ser	Val 285	Leu	Thr	Ile
Asp	Lys 290	Met	Gln	Asn	Lys	Asp 295	Lys	Gly	Leu	Tyr	Thr 300	Cys	Arg	Val	Arg
Ser 305	Gly	Pro	Ser	Phe	Lys 310	Ser	Val	Asn	Thr	Ser 315	Val	His	Ile	Tyr	Asp 320
Lys	Ala	Gly	Pro	Gly 325	Glu	Pro	Lys	Ser	Cys 330	Asp	Lys	Thr	His	Thr 335	Cys
Pro	Pro	Сув	Pro 340	Ala	Pro	Glu	Leu	Leu 345	Gly	Gly	Pro	Ser	Val 350	Phe	Leu
Phe	Pro	Pro 355	Lys	Pro	Lys	Asp	Thr 360	Leu	Met	Ile	Ser	Arg 365	Thr	Pro	Glu
Val	Thr 370	Cys	Val	Val	Val	Asp 375	Val	Ser	His	Glu	Asp 380	Pro	Glu	Val	Lys
Phe 385	Asn	Trp	Tyr	Val	Asp 390	Gly	Val	Glu	Val	His 395	Asn	Ala	Lys	Thr	Lys 400

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
405 410 415

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys 420 425 430

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys 435 440 445

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser 450 455 460

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys 465 470 475 480

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
485 490 495

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly 500 505 510

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln 515 520 525

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn 530 540

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys 545 550 555

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	gtc Val 50			_		_											192
	aag Lys				_		_			_							240
	gac Asp															,	288
	Gly 333		_		_	_	_		_				_		_		336
	aac Asn					_							_				384
	agc Ser 130																432
	aat Asn	_		_				_		_	_	_		_			480
	agt Ser			_	_		_		_				_				528
	tac Tyr	_	_				_		_				_				576
	tat Tyr		_	_	_		_							_			624
acc	tca	gtg	cat	ata	tat	gat	aaa	gca	ggc	ccg	ggc	gag	ccc	aaa	tct		672

Thr	Ser 210	Val	His	Ile	Tyr	Asp 215	Lys	Ala	Gly	Pro	Gly 220	Glu	Pro	Lys	Ser		
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		_		_								aag Lys				768	
												gtg Val				816	
	_	-										gac Asp 285				864	
												tac Tyr				912	
	_		_	_	_							gac Asp				960	
												ctc Leu				1008	
									_	_		cga Arg	_			1056	
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												gac Asp				1152	
			-									aag Lys				1200	
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Met Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu 35 40 45

Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu 50 60

Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile 65 70 75 80

Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu 85 90 95

Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys
100 105 110

Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Gln
115 120 125

Ile Ser Thr Pro Arg Pro Val Lys Leu Leu Arg Gly His Thr Leu Val 130 135 140

Leu Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr Arg Val Gln Met Thr 145 150 155 160

Trp Ser Tyr Pro Asp Glu Ile Asp Gln Ser Asn Ser His Ala Asn Ile

165 170 175

Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys Asp Lys Gly 180 185 190

Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys Ser Val Asn 195 200 205

Thr Ser Val His Ile Tyr Asp Lys Ala Gly Pro Gly Glu Pro Lys Ser 210 215 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu 225 230 235 240

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu 245 250 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser 260 265 270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu 275 280 285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr 290 295 300

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn 305 310 315 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro 325 330 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln 340 345 350

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val 355 360 365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val 370 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro 385 390 395 400

415 405 410 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val 420 425 430 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu 445 435 440 Ser Pro Gly Lys 450 <210> 17 <211> 1389 <212> DNA <213> Artificial <220> <223> Mut3 <220> <221> CDS <222> (1)..(1389) <400> 17 atg gtc agc tac tgg gac acc ggg gtc ctg ctg tgc gcg ctg ctc agc 48 Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser 10 15 1 tgt ctg ctt ctc aca gga tct agt tcc gga ggt aga cct ttc gta gag 96 Cys Leu Leu Thr Gly Ser Ser Ser Gly Gly Arg Pro Phe Val Glu 25 30 20 atg tac agt gaa atc ccc gaa att ata cac atg act gaa gga agg gag 144 Met Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu 35 40 45 ctc gtc att ccc tgc cgg gtt acg tca cct aac atc act gtt act tta 192 Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu 50 60 55 aaa aag ttt cca ctt gac act ttg atc cct gat gga aaa cgc ata atc 240 Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile 75 80 65 70

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr

	_	_	_	_							gca Ala				gaa Glu	288
			_		_	_	_				GJA aaa					336
											atc Ile				caa Gln	384
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											gac Asp				_	720
_		_	_		Āla	Pro	Glu	Leu	Leu	Gly	gga Gly	Pro	Ser	-		768
						_	_			_	atc Ile					816
	_		_	_							gaa Glu					864
											cat His 300					912

						tac Tyr						960
,						gac Asp						1008
						ctc Leu						1056
						cga Arg						1104
						aag Lys 375						1152
						gac Asp						1200
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Met Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu 35 40 45

Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu 50 60

Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile 65 70 75 80

Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu 85 90 95

Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys
100 105 110

Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Gln 115 120 125

Ile Ser Thr Pro Arg Pro Val Lys Leu Leu Arg Gly His Thr Leu Val
130 135 140

Leu Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr Arg Val Gln Met Thr 145 150 155 160

Trp Ser Tyr Pro Asp Glu Lys Asn Lys Arg Ala Ser Val Arg Arg Arg 165 170 175

Ile Asp Gln Ser Asn Ser His Ala Asn Ile Phe Tyr Ser Val Leu Thr 180 185 190

Ile Asp Lys Met Gln Asn Lys Asp Lys Gly Leu Tyr Thr Cys Arg Val 195 200 205

Arg Ser Gly Pro Ser Phe Lys Ser Val Asn Thr Ser Val His Ile Tyr 210 215 220

Asp Lys Ala Gly Pro Gly Glu Pro Lys Ser Cys Asp Lys Thr His Thr 225 230 235 240

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe

245 250 255

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro 260 265 270

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val 275 280 285

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr 290 295 300

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val 305 310 315 320

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys 325 330 335

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser 340 345 350

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro 355 360 365

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val 370 380

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly 385 390 395 400

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp 405 410 415

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
420 425 430

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His 435 440 445

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys 450 455 460

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_		_			act Thr				_	_						336
			_	_	aag Lys	_		_		_						384
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Ile 145	Ile	His	Met	Thr	Glu 150	Gly	Arg	Glu	Leu	Val 155	Ile	Pro	Cys	Arg	Val 160	
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											aca Thr					720
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Asp	Thr 370	Leu	Met	Ile	Ser	Arg 375	Thr	Pro	Glu	Val	Thr 380	Cys	Val	Val	Val	
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								aca Thr								124
								gtc Val 425								129
								tgc Cys								1344
	_			_				tcc Ser				_	_			139
		_						cca Pro								1440
			_					gtc Val								1488
	_				_	_		999 Gly 505			_					1536
	_			_	_	_		gac Asp								1584
_				_	_	-		tgg Trp								1632
_			_			_	_	cac His				_		_	·	1680
		ctg Leu		_			tga									1704

<210> 20

<211> 567

<212> PRT

<213> Artificial

<400> 20

Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser 1 5 10 15

Cys Leu Leu Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys Asp Pro 20 25 30

Glu Leu Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr 35 40 45

Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro 50 55

Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala
65 70 75 80

Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr 85 90 95

Ala Gln Ala Asn His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val 100 105 110

Pro Thr Ser Lys Lys Glu Thr Glu Ser Ala Ile Tyr Ile Phe Ile 115 120 125

Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu 130 · 135 140

Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val
145 150 155 160

Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr 165 170 175

Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe 180 185 190

Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu

195 200 205

Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Lys Asn Lys Asn Ala Ser Val Arg Arg Ile Asp Gln Ser Asn Ser His Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys Ser Val Asn Thr Ser Val His Ile Tyr Asp Lys Ala Gly Pro Gly Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu 435 440 . 445

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg 450 455 460

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys 470 475 480

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp 485 490 495

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys 500 505 510

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser 515 520 525

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser 530 540

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser 545 550 555 560

Leu Ser Leu Ser Pro Gly Lys 565

<210> 21

ì

<211> 1453

<212> DNA

<213> Artificial

<220>

<223> Flt 1 Receptor

<220>

<221> CDS

<222> (69)..(1442)

<400> 21 aagcttgggc tgcaggtcga tcgactctag aggatcgatc cccgggcgag ctcgaattcg	60
caaccacc atg gtc agc tac tgg gac acc ggg gtc ctg ctg tgc gcg ctg Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu 1 5 10	110
ctc agc tgt ctg ctt ctc aca gga tct agt tcc gga ggt aga cct ttc Leu Ser Cys Leu Leu Thr Gly Ser Ser Ser Gly Gly Arg Pro Phe 15 20 25 30	158
gta gag atg tac agt gaa atc ccc gaa att ata cac atg act gaa gga Val Glu Met Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly 35 40 45	206
agg gag ctc gtc att ccc tgc cgg gtt acg tca cct aac atc act gtt Arg Glu Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val 50 55 60	254
act tta aaa aag ttt cca ctt gac act ttg atc cct gat gga aaa cgc Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg 65 70 75	302
ata atc tgg gac agt aga aag ggc ttc atc ata tca aat gca acg tac Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr 80 85 90	350
aaa gaa ata ggg ctt ctg acc tgt gaa gca aca gtc aat ggg cat ttg Lys Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu 95 100 105 110	398
tat aag aca aac tat ctc aca cat cga caa acc aat aca atc ata gat Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp 115 120 125	446
gtg gtt ctg agt ccg tct cat gga att gaa cta tct gtt gga gaa aag Val Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu Lys 130 135 140	494
ctt gtc tta aat tgt aca gca aga act gaa cta aat gtg ggg att gac Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile Asp 145 150 155	542
ttc aac tgg gaa tac cct tct tcg aag cat cag cat aag aaa ctt gta Phe Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys Lys Leu Val 160 165 170	590
aac cga gac cta aaa acc cag tct ggg agt gag atg aag aaa ttt ttg Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe Leu 175 180 185 190	638
agc acc tta act ata gat ggt gta acc cgg agt gac caa gga ttg tac Ser Thr Leu Thr Ile Asp Gly Val Thr Arg Ser Asp Gln Gly Leu Tyr 195 200 205	686
acc tgt gca gca tcc agt ggg ctg atg acc aag aag aac agc aca ttt Thr Cys Ala Ala Ser Ser Gly Leu Met Thr Lys Lys Asn Ser Thr Phe 210 215 220	734

		gtc Val 225													782
	_	cca Pro													830
		aaa Lys													878
		gtg Val													926
		tac Tyr													974
		gag Glu 305													1022
_	_	cac His					_		_					_	1070
		aaa Lys									_			_	1118
		cag Gln		_	_	_									1166
_		ctg Leu						_							1214
		ccc Pro 385	_	_									-		1262
		aac Asn											_		1310
		ctc Leu		-	_			_	_				_	_	1358
		gtc Val			_		_			_	_				1406
	_	cag Gln	_	_		_		_			tgag	gegge	ccg c	2	1453

450 455

<210> 22

<211> 458

<212> PRT

<213> Artificial

<400> 22

Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser 1 5 10 15

Cys Leu Leu Thr Gly Ser Ser Ser Gly Gly Arg Pro Phe Val Glu 20 25 30

Met Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu 35 40 45

Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu 50 60

Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile 65 70 75 80

Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu
85 90 95

Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys
100 105 110

Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Val 115 120 125

Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu Lys Leu Val 130 135 140

Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile Asp Phe Asn 145 150 155 160

Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys Lys Leu Val Asn Arg 165 170 175

Asp	Leu	Lys	Thr 180	Gln	Ser	Gly	Ser	Glu 185	Met	Lys	Lys	Phe	Leu 190	Ser	Thr
Leu	Thr	Ile 195	Asp	Gly	Val	Thr	Arg 200	Ser	Asp	Gln	Gly	Leu 205	Tyr	Thr	Cys
Ala	Ala 210	Ser	Ser	Gly	Leu	Met 215	Thr	Lys	Lys	Asn	Ser 220	Thr	Phe	Val	Arg
Val 225	His	Glu	Lys	Gly	Pro 230	Gly	Asp	Lys	Thr	His 235	Thr	Cys	Pro	Pro	Cys 240
Pro	Ala	Pro	Glu	Leu 245	Leu	Gly	Gly	Pro	Ser 250	Val	Phe	Leu	Phe	Pro 255	Pro
Lys	Pro	Lys	Asp 260	Thr	Leu	Met	Ile	Ser 265	Arg	Thr	Pro	Glu	Val 270	Thr	Cys
Val	Val	Val 275	Asp	Val	Ser	His	Glu 280	Asp	Pro	Glu	Val	Lys 285	Phe	Asn	Trp
Tyr	Val 290	Asp	Gly	Val	Glu	Val 295	His	Asn	Ala	Lys	Thr 300	Lys	Pro	Arg	Glu
Glu 305	Gln	Tyr	Asn	Ser	Thr 310	Tyr	Arg	Val	Val	Ser 315	Val	Leu	Thr	Val	Leu 320
His	Gln	Asp	Trp	Leu 325	Asn	Gly	Lys	Glu	Tyr 330	Lys	Cys	Lys	Val	Ser 335	Asn
Lys	Ala	Leu	Pro 340	Ala	Pro	Ile	Glu	Lys 345	Thr	Ile	Ser	Lys	Ala 350	Lys	Gly
Gln	Pro	Arg 355	Glu	Pro	Gln	Val	Tyr 360	Thr	Leu	Pro	Pro	Ser 365	Arg	Asp	Glu
Leu	Thr 370	Lys	Asn	Gln	Val	Ser 375	Leu	Thr	Cys	Leu	Val 380	Lys	Gly	Phe	Tyr
Pro 385	Ser	Asp	Ile	Ala	Val 390	Glu	Trp	Glu	Ser	Asn 395	Gly	Gln	Pro	Glu	Asn 400
Asn	Tyr	Lys	Thr	Thr 405	Pro	Pro	Val	Leu	Asp 410	Ser	Asp	Gly	Ser	Phe 415	Phe

425 430 420 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr 435 440 Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys 455 450 <210> 23 <211> 1444 <212> DNA <213> Artificial <220> <223> Flt 1 Receptor <220> <221> CDS <222> (69)..(1436) <400> 23 aagettggge tgeaggtega tegaetetag aggategate eeegggegag etegaatteg 60 caaccacc atg gtc agc tac tgg gac acc ggg gtc ctg ctg tgc gcg ctg 110 Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu 10 ctc agc tgt ctg ctt ctc aca gga tct agt tcc gga ggt aga cct ttc 158 Leu Ser Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Gly Arg Pro Phe 30 15 20 206 gta gag atg tac agt gaa atc ccc gaa att ata cac atg act gaa gga Val Glu Met Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly 35 40 45 agg gag ctc gtc att ccc tgc cgg gtt acg tca cct aac atc act gtt 254 Arg Glu Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val 60 50 55 act tta aaa aag ttt cca ctt gac act ttg atc cct gat gga aaa cgc 302 Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

70

65

75

	atc Ile 80											350	·
	gaa Glu											398	
	aag Lys											446	
	cag Gln											494	
	gtc Val											542	
	gac Asp 160											590	
	gag Glu											638	
	atc Ile											686	
_	aac Asn										_	734	
	gaa Glu			_		_						782	
	cct Pro 240											830	
	aag Lys				_							878	
	gtg Val	_		_								926	
	gac Asp		_									974	
	tac Tyr											1022	

305 310 315

						gag Glu								1070
_			_			aaa Lys								1118
						acc Thr							ctg Leu	1166
						acc Thr			_		_	_		1214
						gag Glu 390				_		_		1262
	_					ctg Leu				Gly				1310
	_	_				aag Lys								1358
		_			_	gag Glu	_	_						1406
-	_			_		ggt Gly		tga	gcgg	geege	2			1444

<210> 24

<211> 455

<212> PRT

<213> Artificial

<400> 24

Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser 1 5 10 15

Cys Leu Leu Thr Gly Ser Ser Ser Gly Gly Arg Pro Phe Val Glu 20 25 30

Met Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Ile Gln Leu Leu Pro Arg Lys Ser Leu Glu Leu Leu Val Gly Glu Lys Leu Val Leu Asn Cys Thr Val Trp Ala Glu Phe Asn Ser Gly Val Thr Phe Asp Trp Asp Tyr Pro Gly Lys Gln Ala Glu Arg Gly Lys Trp Val Pro Glu Arg Arg Ser Gln Gln Thr His Thr Glu Leu Ser Ser Ile Leu Thr Ile His Asn Val Ser Gln His Asp Leu Gly Ser Tyr Val Cys Lys Ala Asn Asn Gly Ile Gln Arg Phe Arg Glu Ser Thr Glu Val Ile Val His Glu 

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys 245 250 255

Asn Gly Pro Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val 260 265 270

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp 275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr 290 295 300

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp 305 310 315 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu 325 330 335

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg 340 345 350

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys 355 360 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp 370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys 385 390 395 400

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser 405 410 415

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser 420 425 430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser 435 440 445

Leu Ser Leu Ser Pro Gly Lys
450 455

<210> 25

<211> 1377

<212> DNA

<213> Artificial

<223> Flt 1 Red	ceptor			
<220>				
<221> CDS				
<222> (1)(137	77)			
•				
<400> 25 atg gtc agc tac Met Val Ser Tyr 1				
tgt ctg ctt ctc Cys Leu Leu Leu 20		_		
ttc gta gag atg Phe Val Glu Met 35		Ile Pro Glu	Ile Ile His Met	
gga agg gag ctc Gly Arg Glu Leu 50	_			
gtt act tta aaa Val Thr Leu Lys 65	_	_		
cgc ata atc tgg Arg Ile Ile Trp				
tac aaa gaa ata Tyr Lys Glu Ile 100	-		_	
ttg tat aag aca Leu Tyr Lys Thr 115		_		
gat gtg gtt ctg Asp Val Val Leu 130	_		_	
aag ctt gtc tta Lys Leu Val Leu 145	_	Ala Arg Thr		
gac ttc aac tgg Asp Phe Asn Trp	<del>-</del>		<del>-</del>	

<220>

_		_		Leu			_					atg Met			_	576	
_	_					_		_				gac Asp 205	_	_	_	624	
		_		_		_		_	_			aag Lys				672	
	_		_		_	_	_					tgc Cys				720	
	_		_		_			_		_		ctc Leu				768	
		_	_			_						gag Glu	-			816	
		_				_				_	_	aag Lys 285	_			864	
												aag Lys			_	912	
	_			_	-							ctc Leu	_	_		960	
												aag Lys	_			1008	
	_			_								aaa Lys	_		_	1056	
_		_	_									tcc Ser 365			_	1104	
_		_		_	_	_			_	_	_	aaa Lys				1152	
				_	_							cag Gln				1200	

			cct Pro										1248
	_	_	acc Thr		_	_	-					;	1296
-		_	gtg Val	_			_	_			_	,	1344
_	 _		ctg Leu		_			tga					1377

<210> 26

<211> 458

<212> PRT

<213> Artificial

<400> 26

Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser 1 10 15

Cys Leu Leu Thr Gly Ser Ser Ser Gly Ser Asp Thr Gly Arg Pro 20 25 30

Phe Val Glu Met Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr Glu 35 40 45

Gly Arg Glu Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile Thr 50 55 60

Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys 70 75 80

Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr 85 90 95

Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His
100 105 110

Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile Asp Phe Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys Lys Leu Val Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe Leu Ser Thr Leu Thr Ile Asp Gly Val Thr Arg Ser Asp Gln Gly Leu Tyr Thr Cys Ala Ala Ser Ser Gly Leu Met Thr Lys Lys Asn Ser Thr Phe Val Arg Val His Glu Lys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly 

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu 355 360 365

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr 370 380

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn 385 390 395 400

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe 405 410 415

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn 420 425 430

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr 435 440 445

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys 450 455

<210> 27

<211> 431

<212> PRT

<213> Artificial

<220>

<223> Peptide

<400> 27

Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu Ile Ile His
1 10 15

Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val Thr Ser Pro 20 25 30

Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro 35 40 45

Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser 50 55

Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile Asp Phe Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys Lys Leu Val Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe Leu Ser Thr Leu Thr Ile Asp Gly Val Thr Arg Ser Asp Gln Gly Leu Tyr Thr Cys Ala Ala Ser Ser Gly Leu Met Thr Lys Lys Asn Ser Thr Phe Val Arg Val His Glu Lys Gly Pro Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser

•)

370 375 380

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg 385 390 395 400

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu 405 410 415

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys 420 425 430